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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                               Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atggcttcacccagcctccc.....ttcaggagcatgaagtttga 1362
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1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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em_estpl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11 12	10 9	7 6	5 4	ωΝ	_ ;	ult No.
406.6 386	429.6 413.6 409.2	471.2 464	494.4 479.8	503.6 502.4	508.6	Score
29.9 28.3	31.5 30.4 30.0	34.6 34.1	36.3 35.2	37.0 36.9	37.3	Query Match Length DB
821 387	678 460 690	759 843	814 578	591 534	676	ength 1
11 10	10 10	11	10	10 10	10	
BG752229 AI272281	AI936826 AI937602 AW149665	BF126050 BF125134	AL567376 AI742092	AI884686 BE350014	BE385990	ID
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228.6	١.	240	240	243	249.4	250.4	251.4	264.8	265.6	268.2	268.6	273.2	274.6	278.6	285	287.6	292.6	293	294	299.6	303.6	304.6	305.6	324.8	336.6	341.8	361.6	367.4	371.2	379.8	
16.8																															
313	- U	370	368	476	640	500	367	520	515	395	527	379	549	537	1490	1130	537	561	540	589	558	396	551	433	396	381	696	616	699	645	649
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AI480207	7777777	AW43/808	BF935708	BF072978	AW148557	AW075598	AA780222	BE480975	AI336858	BH045199	AW338938	AI869176	AW652744	AI018769	AK012406	AK016817	BF594242	AW150789	BF939693	AI859538	AA173383	AI499630	BE858216	AW417651	AA613995	AA834860	BF439382	AI990500	BE395581	BF432379	59
AI480207 tm72f01.x	AT423162 +f32c12.x	AA084248 Zn17f09.r	BE933/06 MRZ-NIOL3	BF0/29/8 219508 MA	118	AW075598 xb24e07.x	AA780222 at52g03.s	BE480975 166250 BA	qx86g11	RPCI-24-	ha68h04.	AI869176 W150C05.x	AW652744 101070 MA	69	0	Mus		AW150789 xg39c02.x	w		AA173383 zp04h05.s				-	_		6	8013US	2	590950

ALIGNMENTS

FEATURES SOUTCE	COMMENT	REFERENCE AUTHORS TITLE JOIRNAL	RESULT 1 BE385990/C LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE COCCURT
High quality sequence stop: 653. Location/Qualifiers 1. 676 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="ImAGE:3617696" /clone="ImB-NGIH-MGC_20" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: APCC/DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. CONSORTHUM (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consorthum/LLNL at: image.llnl.gov	Divisional Translatures of Health, Mammalian Gene Collection (MGC) National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	BE385990 676 bp mRNA EST 21-JUL-2000 601276636F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617696 5', mRNA sequence. BE385990 BE385990.1 GI:9331355 EST. BUT.

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REFERENCE
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                                             JOURNAL
                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTCGCTGCAGCACGCCAACCACGAGAAGCGCCTGCGCGTACATGCGCACTCCACCACCG
                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 591)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (1998)
Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                               AI884686
                                                                                                                                                                                                                                                                                                                                                            AI884686 591 bp mRNA EST 07-MAR-2000 w183d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431501 3' similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
                                                                                                                                                                                                                                                                           EST
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99.2%;
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CTGCAGAGAATGGTTTTCANGAGCATGAAGT 590

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ctgcagagaatggttttcaggagcatgaagt 1358
                                                                                     cccagtcattgagtctcgagtcactagagcccaactcaggcgcgaaaccagccaattctg 1327
                                                                                                                                                                                                                                                                                                                                   tgtcgctgcagcacgccaaccacgagaagcgcctgcgcgtacatgcgcactccaccacccg 1147
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                                                           CCCAGTCATTGAGTCTCGAGTCACTAGAGCCCAACTCAGGCGCGAAACCCAGCCAATTCTG
                                                                                                                                          GGAGAACTGAGAAGATTTTCTTAAGCACTTTTCAGAGCGAGGCCGAGCCCCAGTCTAAGT
                                                                                                                                                                ggagaactgagaagattttcttaagcacttttcagagcgaggccgagccccagtctaagt 1267
                                                                                                                                                                                                                                ACAGCGCCCGCTTTGTGCAGCGCCCGTTGCTCTTCGCGTCCCGGCGCCAGTCCTCTGCAA 439
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High quality sequence stop: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1462 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI_CGAP clone distribution information can b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE: 2431501"
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99.0%;
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Pred. No. 2.4e-100;
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                                                                                                                                                                tgtacacggtgtcctcgcagcagtttcggcgggtgttcgtgcaggtgctgtgctgccgcc
                                                                                                                                                                                                                       TGATCCTCCCCTTCTCGGAGACGTTTTCTACCTCAGCTCGGTCATCAACCCGCTCC
                                                                                  tgtcgctgcagcacgccaaccacgagaagcgcctgcgcgtacatgcgcactccaccac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Ph.D. Library Preparation: Life
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      info@image.llnl.gov
Seq primer: -40UP from Gibco
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/clone="TMAGE:3146086"
/clone_11b="NCI_CGAP_Kid13"
/tissue_type="2 pooled Wilms' tumors, one primary and one
metastatic to brain"
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                                                                                                                     908
                                                                                                                                                                             848 tcttcctgaggctgattgttgtgacattggccgtatgctggatgcccaaccagattcgga 907
    206
                                                                                                                                                        86 TYTGCCCAGGGCTGATTGTTGTGACATTGGCCGTATGYTGGATGCCCAACCAGATTTGGA 145
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ggatcatggctgcggccaaacccaagcacgactggacgaggtcctacttccgggcgtaca 967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL567376 814 bp mRNA EST 16-FEB-2001 AL567376 LTI_FL013_FBrn1 Homo sapiens cDNA clone CSODF024Y004
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                               pcmvSpORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
                                                                                                                                                                                                                                                                                                                                                                              http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="pooled tissue from post conception fetuses week, 24 week and 26 week)"
/lab_host="DH10B"
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/clone="CSODF024Y004"
/clone_lib="LTI_FL013_FBrn1"
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96.7%;
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Pred. No. 2.7e-98;
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Seq primer: -400P from Gibco
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/note-Porgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 333208-325895 Soares NbHSF pool 1: 150407, 1511/6-152327 Soares NbHSF-9w pool 1: 758280-760583, 772104-774407 Soares NbHFR-9w pool 1: 304776-306311, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento
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                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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           High quality sequence stop: 723
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                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcgcccgctttgtgcagcgcccgttgctcttcgcgtcccggcgccagtcctctgcaagga 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATGGCTGCGGCCAAACCCAAGCACGACTGGACGAGGTCCTACTTCCGGGCGTACATGA 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGCCCGCTTTGTGCAGCGCCCGTTGCTCTTCGCGTCCCGGCGCCAGTCCTCTGCAAGGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAGAATGGTTTTCAGGAGCATGAAGTTTGA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACACGGTGTCCTCGCAGCAGTTTCGGCGGGTGTTCGTGCAGGTGCTGTGCTGCCGCCTGT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 843)
                                                                                                                                                                                                                                                                              mRNA sequence.
BF125134
                                                                                                                                                                                                                                                                                                                                            BF125134 843 bp mRNA EST 44-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-1-2-U-
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                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                          BF125134.1 GI:10964174
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Directionally (programs skin; Vector: pOTB7; Site_1: XhoI; Site_2: CORI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
91 a 192 c 221 g 155 t
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/db_xref="taxon:9606"
/clone="IMAGE:4026092"
/clone_lib="NH_MGC_20"
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TTCAGGAGCATGAAGTTTGA 16
                                                                                                                                                                         togagtoactagagcccaactcaggcgcgaaaccagccaattctgctgcagagaatggtt 1342
                                                                                                                                                                                                                                                                        TTTTCTTAAGCACTTTTCAGAGCGAGGCCGAGCCCCAGTCTAAGTCCCAGTCATTGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                       TGCAGCGCCCGTTGCTCTCGCGTCCCGGCGCCCAGTCCTCTGCAAGGAGAACTGAGAAGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                      tycagcycccyttyctcttcycytcccyycyccaytcctctycaaygagaactgagaaga 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAACCACGAGAAGCGCCTGCGCGTACATGCGCACTCCACCGACAGCGCCCGCTTTG 214
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                                                                                                                                  TCGAGTCACTAGAGCCC-ACTCAGGCGCGAAACCAGCC-ATTCTGCTGCAGAGAATGGTT
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Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_most="DH10B (phage-resistant)"
/lab_most="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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99.48;
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Pred. No. 1.3e-91;
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1028 tgtacacggtgtcctcgcagcagtttcggcgggtgttcgtgcaggtgctgtgctgtccccc
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                                                                                                                                                                                                                                                848 tcttcctgaggctgattgttgtgacattggccgtatgctggatgcccaaccagattcgga 907
                                                                                                                                                                  ggatcatggctgcggccaaaccccaagcacgactggacgaggtcctacttccgggcgtaca 967
                                                               TGATCCTCCTCCCCTTCTCGGAGACGTTTTTCTACCTCAGCTCGGTCATCAACCCGCTCC 418
                                                                                    tgatcctcctccccttctcggagacgtttttctacctcagctcggtcatcaacccgctcc
                                                                                                                                             GGATCATGGCTGCGGCCAAACCCAAGCACGACTGGACGAGGTCCTACTTCCGGGCGTACA 358
                                                                                                                                                                                                                             TCTGCCCAGGGCTGATTGTTGTGACATTGGCCGTATGCTGGATGCCCAACCAGATTCGGA 298
                                                                                                                                                                                                                                                                                                             432;
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Seq primer: -40UP from Gibco
High quality sequence stop: 454.
Location/Qualifiers
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Insert Length: 1143 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AI936826
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
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                                                                                                                                                                                                                                                                                                           Conservative
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone="IMAGE:2467075"
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Pred. No. 4.1e-84;
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1 (bases 1 to 460)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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Seq primer: -40UP from Gibco
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2468197"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1281 tctcgagtcactagagcccaactcaggcgcgaaaccagcc 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1161 tgtgcadcgcccgttgctcttcgcgtccccggcgccagtcctctgcaaggagaactgagaa 1220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CTTCTCGGAGACGTTTTCTACCTCAGCTCGGTCATCAACCCGCTCCTGTACACGGTGTC
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                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 690)

21 (bases 1 to 690)

RS NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consorthum/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCAACCACGAGAAGCGCCTGCGCGTACATGCGCACTCCACCACCGACAGCGCCCGCTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW149665 690 bp mRNA EST 03-NOV-1999 xf40h05.x1 NCI_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2620569 3' similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wrx39.;, mRNA sequence.
AW149665
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                                                               Possible reversed clone: similarity on wrong strand Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                        High quality sequence stop: 402.
                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                           KEYWORDS
                                                       AUTHORS
TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                848 tottcotgaggotgattgttgtgacattggcogtatgctggatgcccaaccagattcgga 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGATCCTCCTCCCCTTCTCGGAGACGTTTTTCTACCTCAGCTCGGTCATCAACCCGCTCC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgatcctcctccccttctcggagacgtttttctacctcagctcggtcatcaaccagctcc 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGAACTGAGAAGATNTTCTTAAGCACCTTTCAGAACGAAGCCGAGCCCCAAGTCTAAT 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggagaactgagaagattttcttaagcacttttcagagcggaggccgagccccagtctaagt 1267
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                                                                                                                                                                                                                                                                                                                                                                                           TCCAGTCATTGAATTTCGA 689
                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 821)
                                                                                                                                                                                                                                mRNA sequence.
BG752229
                                                                                                                                                                                                                                                                      BG752229 821 bp mRNA
602731372F1 NIH_MGC_43 Homo
                  Contact: Robert Strausberg, Ph.D
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                  BG752229.1
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             medulloblastoma tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is normalized. Library constructed by Bento Soares and M. Fatima Bonaldo. " 196 c 160 g 191 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2630569"
/clone=lib="NCI_CGAP_Brn50"
/tissue_type="medulloblastoma"
/lab_host="DH10B (phage resistant)"
/nate="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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95.7%;
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Pred. No. 1.2e-79;
                                                                                                                                                                                                                                                                                                mRNA
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                                                             Gene Collection (MGC)
                                                                                                                     Hominidae;
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RESULT 12
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Best Local :
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                                                                                                                                                     326 CTGCAGAGAATGGTTTTCAGGAGCATGAAGTTTGA 292
                                                                                                                                                                                                                                                                           386 AATTCAATTGGATTCTCGAGTCACTAGAGCCCAACTCAGGCGCGAAACCAGCCAATTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tccccttctcggagacgtttttctacctcagctcggtcatcaacccgctcctgtacacgg 1036
   AI272281
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Plate: LLCM1755 row: o column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_43"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_nost="PullOB (phage-resistant)"
/lab_nost="PullOB (phage-resistant)"
/lab_nost="PullOB (phage-resistant)"
/lab_nost="Normal pigmented polity"
/lab_nost="Normal pigmented"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/coned into Econt/XhoI sites using the following 5'
cloned into Econt/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC Library. | "
An 2011 2018 TIR TOTAL
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/db_xref="taxon:9606"
/clone="IMAGE:4875113"
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                             1042
                                                                                                                                                                                                327 GCCAAACCCAAGCACGACTGGACGAGGTCCTACTTCCGGGCGTACATGATCCTCCTCCCC
                                                                                                                                                                                                                                                                                                              387 ATTGTTGTGACATTGNCCGTATGCTGGATGCCCAACCAGATTCGGAGGATCATGGCTGCG
                                                                                                                                                                                                                                                                                                                                                                   862 attgttgtgacattggccgtatgctggatgcccaaccagattcggaggatcatggctgcg 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
tcgcagcagtttcggcgggtgttcgtgcaggtgctgtgctgccgcctgtcgctgcagcac
                                                                                                           ttctcggagacgtttttctacctcagctcggtcatcaacccgctcctgtacacggtgtcc 1041
                                                                                                                                                                                                                          gccaaacccaagcactggacgaggtcctacttccgggcgtacatgatcctcctcccc
                                                                                    TTCTCGGAGACGTTTTTCTACCTCAGCTCGGTCATCAACCCGCTCCTGTACACGGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washd,NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found Strand Possible reversed clone: polyT not found Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Wilson RK
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AI272281.1 GI:3894552
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inote-*Organ: brain; Vector: pBluescript SK- (Stratagene); Site_1: EcoRI; Site_2: XhoI; Double-Stranded cDNA was prepared from human oligodendroglioma using primer 5'-GAGAGAGAGAGAGAGAGAGAGAGAGTCTGAGT(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATTCGGCAGGAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology; contains chromosome 1p and 19q deletion as determined by CGH. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library was constructed by Dr. Martin Schiller (Johns Hopkins University)."
103 c 127 g 69 t 1 others
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/clone="IMAGE:1956196"
/clone_lib="Schiller oligodendroglioma"
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/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 386; DB 10;
Pred. No. 1.3e-74;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW590950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity on wrong strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Cancer Institute, Cancer Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        image.linl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: NCI-CGAP clone distribution ound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 649)
                                                                                                                                           132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: -40UP from Gibco
         Conservative
                                                                                                                                    note="Vector: pM7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PGR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 125096-125831, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "a 189 c 155 g 173 t
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2949166"
/clone_lib="NCI_CGAP_GC6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                         28.1%;
97.3%;
       0,
                         Score 383; DB 10;
Pred. No. 6.6e-74;
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       Mismatches
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Gaps
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1 (bases 1 to 645)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                   Seq primer: -400\bar{P} from Gibco High quality sequence stop: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CGAP/BTGAP), Tumo
Unpublished (1998)
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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                                                                                                                                                                                                                              quality sequence stop: 441.
Location/Qualifiers
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                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3406292"
/clone_lib="NOI_CGAP_Brn23"
/tissue_type="glioblastoma (p
/lab_host="DH108"
Ph.D.
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                                                                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                        http://image.llnl.gov
Plate: LLCM320 row: l column:
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                                                                                quality sequence stop: 579.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                            Location/Qualifiers
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                                                                 gtttga 1362
                                                                                                                                                                                                                                                                                                 TTTCAGAGCGAGGCCGAGCCCCAGTCTAAGTCCCAGTCATTGAGTCTCGAGTCACTAGAG
                                                                                                                                                                                                                                                                                                                                    tttcagagcgaggccgagccccagtctaagtcccagtcattgagtctcgagtcactagag 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTTCGCGTCCCGGCGCCAGTCCTCTGCAAGGAGAACTGAGAAGATTTTCTTAAGCACT
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/clone_lib="NIH_MGC.44"
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/lab_host="DH1DB (phage-resistant)"
/lab_host="DH1DB (phage-resistant)"
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Pred. No. 2.6e-71;
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